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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/970,969

DATE: 10/19/2001

TIME: 10:33:27

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10192001\I970969.raw

3 <110> APPLICANT: Tait, Jonathan F.
5 Brown, David S.
9 <120> TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
13 <130> FILE REFERENCE: uofw-1-13841
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/970,969
C--> 19 <141> CURRENT FILING DATE: 2001-10-03
23 <160> NUMBER OF SEQ ID NOS: 6
27 <170> SOFTWARE: PatentIn Ver. 2.0
31 <210> SEQ ID NO: 1
33 <211> LENGTH: 981
35 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
41 <220> FEATURE:
43 <221> NAME/KEY: CDS
45 <222> LOCATION: (1)..(981)
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59 act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg 96
61 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg
63 20 25 30
67 aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg 144
69 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
71 35 40 45
75 ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192
77 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
79 50 55 60
83 aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta 240
85 Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
87 65 70 75 80
91 act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg 288
93 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
95 85 90 95
99 ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336
101 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
103 100 105 110
107 aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa 384
109 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
111 115 120 125
115 ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg 432
117 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
119 130 135 140
123 gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg 480
125 Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
127 145 150 155 160
131 gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa 528

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135                               165                               170                               175
139 gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt 576
141 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
143                               180                               185                               190
147 aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga 624
149 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
151                               195                               200                               205
155 agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca 672
157 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
159                               210                               215                               220
163 gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta 720
165 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
167 225                               230                               235                               240
171 gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc 768
173 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
175                               245                               250                               255
179 tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat 816
181 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
183                               260                               265                               270
187 gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg 864
189 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
191                               275                               280                               285
195 ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat 912
197 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
199                               290                               295                               300
203 tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960
205 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
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213 Leu Leu Ser Gly Glu Asp Asp
215                               325
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225 <212> TYPE: PRT
227 <213> ORGANISM: Homo sapiens
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245 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
247 35 40 45
251 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
253 50 55 60
257 Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
259 65 70 75 80
263 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
265 85 90 95

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271      100      105      110
275 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
277      115      120      125
281 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
283      130      135      140
287 Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
289 145      150      155      160
293 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
295      165      170      175
299 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
301      180      185      190
305 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
307      195      200      205
311 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
313      210      215      220
317 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
319 225      230      235      240
323 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
325      245      250      255
329 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
331      260      265      270
335 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
337      275      280      285
341 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
343      290      295      300
347 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
349 305      310      315      320
353 Leu Leu Ser Gly Glu Asp Asp
355      325
361 <210> SEQ ID NO: 3
363 <211> LENGTH: 981
365 <212> TYPE: DNA
367 <213> ORGANISM: Homo sapiens
371 <220> FEATURE:
373 <221> NAME/KEY: CDS
375 <222> LOCATION: (1)..(981)
379 <400> SEQUENCE: 3
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383 Met Ala Gly Gly Cys Gly His Met Ala Gln Val Leu Arg Gly Thr Val
385 1 5 10 15
389 act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg 96
391 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg
393 20 25 30
397 aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg 144
399 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
401 35 40 45
405 ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192
407 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe

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417 65      70      75      80
421 act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg 288
423 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
425      85      90      95
429 ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336
431 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
433      100      105      110
437 aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa 384
439 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
441      115      120      125
445 ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg 432
447 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
449      130      135      140
453 gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg 480
455 Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
457 145      150      155      160
461 gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa 528
463 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
465      165      170      175
469 gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt 576
471 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
473      180      185      190
477 aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga 624
479 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
481      195      200      205
485 agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca 672
487 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
489      210      215      220
493 gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta 720
495 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
497 225      230      235      240
501 gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc 768
503 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
505      245      250      255
509 tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat 816
511 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
513      260      265      270
517 gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg 864
519 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
521      275      280      285
525 ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat 912
527 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
529      290      295      300
533 tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960
535 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
537 305      310      315      320

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541 ctg ctc tcc gga gaa gat gac          981
543 Leu Leu Ser Gly Glu Asp Asp
545          325
551 <210> SEQ ID NO: 4
553 <211> LENGTH: 327
555 <212> TYPE: PRT
557 <213> ORGANISM: Homo sapiens
561 <400> SEQUENCE: 4
563 Met Ala Gly Gly Cys Gly His Met Ala Gln Val Leu Arg Gly Thr Val
565   1          5          10          15
569 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg
571          20          25          30
575 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
577          35          40          45
581 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
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587 Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
589          65          70          75          80
593 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
595          85          90          95
599 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
601          100          105          110
605 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
607          115          120          125
611 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
613          130          135          140
617 Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
619 145          150          155          160
623 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
625          165          170          175
629 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
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635 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
637          195          200          205
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643          210          215          220
647 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
649 225          230          235          240
653 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
655          245          250          255
659 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
661          260          265          270
665 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
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671 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
673          290          295          300
677 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
679 305          310          315          320
683 Leu Leu Ser Gly Glu Asp Asp

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VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Application Number

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date